AMENDMENTS

In the Claims:

Claims 1-31. (Canceled)

32. (Previously presented) The method of claim 63, 84, 85, 88, or 106 wherein at least 50% by weight of all proteins in the sample are removed.

Claims 33-51. (Canceled)

52. (Previously presented) The method of claim 63, 84, or 85, further comprising the step of analyzing a plurality of proteins remaining in the modified sample.

Claims 53-61. (Canceled)

62. (Previously Presented) The method of claim 63, 84, or 85, wherein at least one of the proteins is present at higher abundance than at least one of the plurality of proteins remaining in the sample after removal of the proteins.

63. (**Currently Amended**) A method for producing **and recovering** a modified sample, said method comprising:

removing at least a first protein and a second protein from a sample, said removing step comprising contacting said sample with an affinity binding composition

comprising a first solid phase matrix with a first receptor immobilized thereon capable of specific binding to said first protein but not said second protein and a second solid phase matrix with a second receptor immobilized thereon capable of specific binding to said second protein but not said first protein, wherein each said solid phase matrix is a plurality of particles and said first and second solid phase matrices are present as a mixture in said binding composition;

so that when said sample is contacted with said affinity binding composition, said first protein present in said sample binds to said first receptor present on said first solid phase matrix such that said first protein is removed from said sample and said second protein present in said sample binds to said second receptor present on said second solid phase matrix such that said second protein is removed from said sample and said modified sample is thereby produced, wherein said modified sample is not bound by a solid phase matrix; and

recovering said modified sample.

64. (Previously presented) The method of claim 63, wherein the affinity binding composition further comprises:

a third receptor immobilized on a third solid phase matrix, capable of specific binding to a third protein but not the first protein or the second protein.

65. (Previously presented) The method of claim 64, wherein the third solid phase matrix contacts the first and second solid phase matrices.

66. (Previously presented) The method of claim 63, wherein the affinity binding composition further comprises:

a fourth receptor immobilized on a fourth solid phase matrix, capable of specific binding to a fourth protein but not the first protein, the second protein or the third protein.

67. (Previously presented) The method of claim 66, wherein the fourth solid phase matrix contacts the first, second, and third solid phase matrices.

68. (Previously presented) The method of claim 67, wherein the affinity binding composition further comprises:

a fifth receptor immobilized on a fifth solid phase matrix, capable of specific binding to a protein but not the first protein, the second protein, the third protein or the fourth protein.

69. (Previously presented) The method of claim 68, wherein the fifth solid phase matrix contacts the first, second, third, and fourth solid phase matrices.

Claims 70-83. (Canceled)

84. **(Currently Amended)** A method for producing **and recovering** a modified sample, said method comprising:

removing at least a first protein and a second protein from a sample, said removing step comprising contacting said sample with an affinity binding composition comprising a plurality of solid phase matrices with a plurality of receptors having different protein binding specificities immobilized thereon such that each solid phase matrix has a different protein binding specificity, wherein each said solid phase matrix is a plurality of particles and said ~~first and second~~ **plurality of** solid phase matrices are present as a mixture in said binding composition,

so that when said sample is contacted with said affinity binding composition, said at least two proteins become bound to said affinity binding composition and said proteins are thereby removed from the sample such that the modified sample is produced, wherein said modified sample is not bound by a solid phase matrix; and

recovering said modified sample.

85. (Previously presented) The method of claim 63, or 84, wherein the sample is passed through a column containing the affinity binding composition to produce the modified sample, wherein the affinity column has a fluid inlet and a fluid outlet, and wherein the modified sample is collected at the fluid outlet.

Claims 86-87. (Canceled)

88. (Previously Presented) The method of claim 63, 84, or 85, wherein the receptors are antibodies or antibody fragments that specifically bind to the proteins.

89. (Previously presented) The method of claim 63, 84, or 85, wherein the receptors are recombinantly produced.

Claims 90-103. (Canceled)

104. **(Currently Amended)** The method of claim 63, 84, or 85, wherein at least one of the ~~particular~~ proteins is selected from the group consisting of: immunoglobulins, albumin, transferrin, haptoglobin, α_1-antitrypsin, hemopexin, α_1-acid glycoprotein, α2 HS glycoprotein, myosin, transthyretin, α_1-antichymotrypsin, apolipoprotein AI, α_2-macroglobulin, fibrinogen, and prealbumin, and combinations thereof.

105. (Previously Presented) The method of claim 63, 84, or 85, wherein at least two of the proteins are selected from the group consisting of: immunoglobulins, albumin, transferrin, haptoglobin, α_1-antitrypsin, hemopexin, α_1-acid glycoprotein, α2 HS glycoprotein, myosin, transthyretin, α_1-antichymotrypsin, apolipoprotein Al, α_2-macroglobulin, fibrinogen, and prealbumin.

106. (Previously Presented) The method of claim 63, 84, 85, or 88, wherein at least three of the proteins are selected from the group consisting of: immunoglobulins, albumin, transferrin, haptoglobin, α_1-antitrypsin, hemopexin, α_1-acid glycoprotein, α2 HS glycoprotein, myosin, transthyretin, α_1-antichymotrypsin, apolipoprotein Al, α_2-macroglobulin, fibrinogen, and prealbumin.

107. (Previously Presented) The method of claim 63, 84, or 85, wherein at least four of the proteins are selected from the group consisting of: immunoglobulins, albumin, transferrin, haptoglobin, α_1-antitrypsin, hemopexin, α_1-acid glycoprotein, α2 HS glycoprotein, myosin, transthyretin, α_1-antichymotrypsin, apolipoprotein Al, α_2-macroglobulin, fibrinogen, and prealbumin.

Claims 108 - 109. (Canceled)

110. (Previously Presented) The method of claim 63, wherein at least three proteins are removed from a sample.

111. (**Currently Amended**) The method of claim 84, wherein at least ~~the~~ **three** proteins are removed from a sample.

112. (Previously Presented) The method of claim 63, wherein at least four proteins are removed from a sample.

113. (Previously Presented) The method of claim 84, wherein at least four proteins are removed from a sample.